



SEQUENCE LISTING

<110> M&E Biotech A/S

<120> Method for down-regulating GDF-8 activity

<130> AutoVacGDF-8 DK 1

<160> 23

<170> PatentIn Ver. 2.1

<210> 1

<211> 375

<212> PRT

<213> Homo sapiens

<400> 1

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Val	Glu	Lys	Glu	Gly	Leu	Cys	Asn	Ala	Cys	Thr	Trp	Arg	Gln	Asn	Thr
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Lys	Ser	Ser	Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu
	50					55				60					
Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Val	Ile	Arg	Gln	Leu
65					70					75					80
Leu	Pro	Lys	Ala	Pro	Pro	Leu	Arg	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val
				85					90					95	
Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His
			100					105						110	
Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu
			115				120					125			
Met	Gln	Val	Asp	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser
	130					135					140				
Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu
145					150					155					160
Arg	Pro	Val	Glu	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu
				165					170					175	
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu
			180					185					190		
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val
		195					200					205			

Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
 210 215 220
 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
 225 230 235 240
 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
 245 250 255
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
 260 265 270
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
 305 310 315 320
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
 325 330 335
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
 355 360 365
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 2
 <211> 362
 <212> PRT
 <213> Meleagris gallopavo

<400> 2
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 Thr Glu Asn Ala Glu Lys Asp Gly Leu Cys Asn Ala Cys Thr Trp Arg
 20 25 30
 Gln Asn Thr Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu
 35 40 45
 Ser Lys Leu Arg Leu Glu Gln Ala Pro Asn Ile Ser Arg Asp Val Ile
 50 55 60
 Lys Gln Leu Leu Pro Lys Ala Pro Pro Leu Gln Glu Leu Ile Asp Gln
 65 70 75 80
 Tyr Asp Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp

85					90					95					
Asp	Tyr	His	Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser
			100					105					110		
Asp	Phe	Leu	Val	Gln	Met	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys
		115					120					125			
Phe	Ser	Ser	Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp
	130					135					140				
Ile	Tyr	Leu	Arg	Gln	Val	Gln	Lys	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile
145					150					155					160
Leu	Arg	Leu	Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile
			165						170					175	
Arg	Ser	Leu	Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser
		180						185					190		
Ile	Asp	Val	Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser
	195						200					205			
Asn	Leu	Gly	Ile	Glu	Ile	Lys	Ala	Phe	Asp	Glu	Asn	Gly	Arg	Asp	Leu
	210					215					220				
Ala	Val	Thr	Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu
225					230					235					240
Glu	Val	Arg	Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly
			245						250					255	
Leu	Asp	Cys	Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro
		260						265					270		
Leu	Thr	Val	Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro
	275						280					285			
Lys	Arg	Tyr	Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe
	290					295					300				
Leu	Gln	Lys	Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg
305					310					315					320
Gly	Ser	Ala	Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn
			325						330					335	
Met	Leu	Tyr	Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro
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Ala	Met	Val	Val	Asp	Arg	Cys	Gly	Cys	Ser						
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<210> 3
 <211> 375
 <212> PRT

<213> Gallus sp.

<400> 3

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Ala	Val	Asp	Pro	Val	Ala	Leu	Asp	Gly	Ser	Ser	Gln	Pro	Thr	Glu	Asn
			20					25					30		
Ala	Glu	Lys	Asp	Gly	Leu	Cys	Asn	Ala	Cys	Thr	Trp	Arg	Gln	Asn	Thr
		35					40					45			
Lys	Ser	Ser	Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu
	50					55					60				
Arg	Leu	Glu	Gln	Ala	Pro	Asn	Ile	Ser	Arg	Asp	Val	Ile	Lys	Gln	Leu
65					70					75					80
Leu	Pro	Lys	Ala	Pro	Pro	Leu	Gln	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val
				85					90					95	
Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His
		100						105					110		
Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu
		115					120						125		
Val	Gln	Met	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser
	130					135					140				
Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu
145					150					155					160
Arg	Gln	Val	Gln	Lys	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu
				165					170					175	
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu
		180						185					190		
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val
	195						200					205			
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly
	210					215					220				
Ile	Glu	Ile	Lys	Ala	Phe	Asp	Glu	Thr	Gly	Arg	Asp	Leu	Ala	Val	Thr
225					230					235					240
Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Arg
				245					250					255	
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys
			260					265					270		
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val
		275					280					285			

Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
 305 310 315 320
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
 325 330 335
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
 355 360 365
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 4
 <211> 376
 <212> PRT
 <213> Mus musculus

<400> 4
 Met Met Gln Lys Leu Gln Met Tyr Val Tyr Ile Tyr Leu Phe Met Leu
 1 5 10 15
 Ile Ala Ala Gly Pro Val Asp Leu Asn Glu Gly Ser Glu Arg Glu Glu
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 Asn Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Ala Trp Arg Gln Asn
 35 40 45
 Thr Arg Tyr Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys
 50 55 60
 Leu Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln
 65 70 75 80
 Leu Leu Pro Arg Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp
 85 90 95
 Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr
 100 105 110
 His Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe
 115 120 125
 Leu Met Gln Ala Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser
 130 135 140
 Ser Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr
 145 150 155 160
 Leu Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg
 165 170 175

Leu Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser
180 185 190

Leu Lys Leu Asp Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp
195 200 205

Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu
210 215 220

Gly Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val
225 230 235 240

Thr Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val
245 250 255

Lys Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp
260 265 270

Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr
275 280 285

Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg
290 295 300

Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln
305 310 315 320

Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser
325 330 335

Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu
340 345 350

Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met
355 360 365

Val Val Asp Arg Cys Gly Cys Ser
370 375

<210> 5

<211> 375

<212> PRT

<213> Bos taurus

<400> 5

Met Gln Lys Leu Gln Ile Ser Val Tyr Ile Tyr Leu Phe Met Leu Ile
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Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
20 25 30

Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Leu Trp Arg Glu Asn Thr
35 40 45

Thr Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu

50	55	60
Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu		
65	70	75 80
Leu Pro Lys Ala Pro Pro Leu Leu Glu Leu Ile Asp Gln Phe Asp Val		
	85	90 95
Gln Arg Asp Ala Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His		
	100	105 110
Ala Arg Thr Glu Thr Val Ile Thr Met Pro Thr Glu Ser Asp Leu Leu		
	115	120 125
Thr Gln Val Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser		
	130	135 140
Lys Ile Gln Tyr Asn Lys Leu Val Lys Ala Gln Leu Trp Ile Tyr Leu		
145	150	155 160
Arg Pro Val Lys Thr Pro Ala Thr Val Phe Val Gln Ile Leu Arg Leu		
	165	170 175
Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu		
	180	185 190
Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val		
	195	200 205
Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly		
	210	215 220
Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr		
225	230	235 240
Phe Pro Glu Pro Gly Glu Asp Gly Leu Thr Pro Phe Leu Glu Val Lys		
	245	250 255
Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys		
	260	265 270
Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val		
	275	280 285
Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr		
	290	295 300
Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys		
305	310	315 320
Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala		
	325	330 335
Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr		
	340	345 350
Phe Asn Gly Glu Gly Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val		

355

360

365

Val Asp Arg Cys Gly Cys Ser
370 375

<210> 6

<211> 375

<212> PRT

<213> Ovis sp.

<400> 6

Met Gln Lys Leu Gln Ile Phe Val Tyr Ile Tyr Leu Phe Met Leu Leu
1 5 10 15

Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
20 25 30

Val Glu Lys Lys Gly Leu Cys Asn Ala Cys Leu Trp Arg Gln Asn Asn
35 40 45

Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
50 55 60

Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu
65 70 75 80

Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
85 90 95

Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
100 105 110

Val Thr Thr Glu Thr Val Ile Thr Met Pro Thr Glu Ser Asp Leu Leu
115 120 125

Ala Glu Val Gln Glu Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
130 135 140

Lys Ile Gln His Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
145 150 155 160

Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
165 170 175

Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
180 185 190

Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
195 200 205

Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
210 215 220

Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
225 230 235 240

Phe Pro Glu Pro Gly Glu Glu Gly Leu Asn Pro Phe Leu Glu Val Lys
 245 250 255
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
 260 265 270
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Leu Phe Leu Gln Lys
 305 310 315 320
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Lys Gly Ser Ala
 325 330 335
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Gly Met Val
 355 360 365
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 7
 <211> 376
 <212> PRT
 <213> Rattus norvegicus

<400> 7
 Met Ile Gln Lys Pro Gln Met Tyr Val Tyr Ile Tyr Leu Phe Val Leu
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 Ile Ala Ala Gly Pro Val Asp Leu Asn Glu Asp Ser Glu Arg Glu Ala
 20 25 30
 Asn Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Ala Trp Arg Gln Asn
 35 40 45
 Thr Arg Tyr Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys
 50 55 60
 Leu Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln
 65 70 75 80
 Leu Leu Pro Arg Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp
 85 90 95
 Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr
 100 105 110
 His Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe
 115 120 125

Leu Met Gln Ala Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser
 130 135 140
 Ser Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr
 145 150 155 160
 Leu Arg Ala Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg
 165 170 175
 Leu Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser
 180 185 190
 Leu Lys Leu Asp Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp
 195 200 205
 Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu
 210 215 220
 Gly Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val
 225 230 235 240
 Thr Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val
 245 250 255
 Lys Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp
 260 265 270
 Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr
 275 280 285
 Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg
 290 295 300
 Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln
 305 310 315 320
 Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser
 325 330 335
 Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu
 340 345 350
 Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met
 355 360 365
 Val Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 8

<211> 375

<212> PRT

<213> Sus scrofa

<400> 8

Met Gln Lys Leu Gln Ile Tyr Val Tyr Ile Tyr Leu Phe Met Leu Ile

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Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn	20	25	30
Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Met Trp Arg Gln Asn Thr	35	40	45
Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu	50	55	60
Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu	65	70	75
Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val	85	90	95
Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His	100	105	110
Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Leu Leu	115	120	125
Met Gln Val Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser	130	135	140
Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu	145	150	155
Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu	165	170	175
Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu	180	185	190
Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val	195	200	205
Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly	210	215	220
Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr	225	230	235
Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys	245	250	255
Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys	260	265	270
Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val	275	280	285
Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr	290	295	300
Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys			

305 310 315 320
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
 325 330 335
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
 355 360 365
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 9
 <211> 374
 <212> PRT
 <213> Danio rerio

<400> 9
 Met His Phe Thr Gln Val Leu Ile Ser Leu Ser Val Leu Ile Ala Cys
 1 5 10 15
 Gly Pro Val Gly Tyr Gly Asp Ile Thr Ala His Gln Gln Pro Ser Thr
 20 25 30
 Ala Thr Glu Glu Ser Glu Leu Cys Ser Thr Cys Glu Phe Arg Gln His
 35 40 45
 Ser Lys Leu Met Arg Leu His Ala Ile Lys Ser Gln Ile Leu Ser Lys
 50 55 60
 Leu Arg Leu Lys Gln Ala Pro Asn Ile Ser Arg Asp Val Val Lys Gln
 65 70 75 80
 Leu Leu Pro Lys Ala Pro Pro Leu Gln Gln Leu Leu Asp Gln Tyr Asp
 85 90 95
 Val Leu Gly Asp Asp Ser Lys Asp Gly Ala Val Glu Glu Asp Asp Glu
 100 105 110
 His Ala Thr Thr Glu Thr Ile Met Thr Met Ala Thr Glu Pro Asp Pro
 115 120 125
 Ile Val Gln Val Asp Arg Lys Pro Lys Cys Cys Phe Phe Ser Phe Ser
 130 135 140
 Pro Lys Ile Gln Ala Asn Arg Ile Val Arg Ala Gln Leu Trp Val His
 145 150 155 160
 Leu Arg Pro Ala Glu Glu Ala Thr Thr Val Phe Leu Gln Ile Ser Arg
 165 170 175
 Leu Met Pro Val Lys Asp Gly Gly Arg His Arg Ile Arg Ser Leu Lys
 180 185 190

Ile Asp Val Asn Ala Gly Val Thr Ser Trp Gln Ser Ile Asp Val Lys
 195 200 205
 Gln Val Leu Thr Val Trp Leu Lys Gln Pro Glu Thr Asn Arg Gly Ile
 210 215 220
 Glu Ile Asn Ala Tyr Asp Ala Lys Gly Asn Asp Leu Ala Val Thr Ser
 225 230 235 240
 Thr Glu Thr Gly Glu Asp Gly Leu Leu Pro Phe Met Glu Val Lys Ile
 245 250 255
 Ser Glu Gly Pro Lys Arg Ile Arg Arg Asp Ser Gly Leu Asp Cys Asp
 260 265 270
 Glu Asn Ser Ser Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp
 275 280 285
 Phe Glu Asp Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys
 290 295 300
 Ala Asn Tyr Cys Ser Gly Glu Cys Asp Tyr Met Tyr Leu Gln Lys Tyr
 305 310 315 320
 Pro His Thr His Leu Val Asn Lys Ala Ser Pro Arg Gly Thr Ala Gly
 325 330 335
 Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe
 340 345 350
 Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ser Met Val Val
 355 360 365
 Asp Arg Cys Gly Cys Ser
 370

<210> 10
 <211> 375
 <212> PRT
 <213> Papio hamadryas

<400> 10
 Met Gln Lys Leu Gln Leu Cys Val Tyr Ile Tyr Leu Phe Met Leu Ile
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 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
 20 25 30
 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
 35 40 45
 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 50 55 60
 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu
 65 70 75 80

Leu	Pro	Lys	Ala	Pro	Pro	Leu	Arg	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val	85	90	95
Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	100	105	110
Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu	115	120	125
Met	Gln	Val	Asp	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	130	135	140
Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	145	150	155
Arg	Pro	Val	Glu	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	165	170	175
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	180	185	190
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	195	200	205
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	210	215	220
Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr	225	230	235
Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Lys	245	250	255
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	260	265	270
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	275	280	285
Asp	Phe	Glu	Ala	Leu	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	290	295	300
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys	305	310	315
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala	325	330	335
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr	340	345	350
Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met	Val	355	360	365
Val	Asp	Arg	Cys	Gly	Cys	Ser										370	375	

<210> 11
<211> 109
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)..(109)
<223> Identical to residues 267-375 in SEQ ID NO: 1

<400> 11
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys
1 5 10 15
Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile
20 25 30
Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu
35 40 45
Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala
50 55 60
Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser
65 70 75 80
Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly
85 90 95
Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser
100 105

<210> 12
<211> 109
<212> PRT
<213> Bos taurus

<220>
<221> PEPTIDE
<222> (1)..(109)
<223> Identical to residues 267-375 in SEQ ID NO: 5

<400> 12
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys
1 5 10 15
Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile
20 25 30
Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu
35 40 45
Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala
50 55 60

Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser
65 70 75 80

Pro Ile Asn Met Leu Tyr Phe Asn Gly Glu Gly Gln Ile Ile Tyr Gly
85 90 95

Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser
100 105

<210> 13

<211> 15

<212> PRT

<213> Clostridium tetani

<400> 13

Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
1 5 10 15

<210> 14

<211> 21

<212> PRT

<213> Clostridium tetani

<400> 14

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
1 5 10 15

Ala Ser His Leu Glu
20

<210> 15

<211> 109

<212> PRT

<213> Artificial sequence

<220>

<221> MUTAGEN

<222> (18)..(32)

<223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>

<221> SIMILAR

<222> (1)..(17)

<223> Identical to residues 267-283 in SEQ ID NO: 1

<220>

<221> SIMILAR

<222> (33)..(109)

<223> Identical to residues 299-375 in SEQ ID NO: 1

<220>

<221> SITE

<222> (73)

<223> Cys or Ser

<220>

<221> SITE

<222> (90)..(91)

<223> Lys Glu or Glu Gly

<400> 15

Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys
1 5 10 15

Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
20 25 30

Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu
35 40 45

Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala
50 55 60

Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser
65 70 75 80

Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly
85 90 95

Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser
100 105

<210> 16

<211> 109

<212> PRT

<213> Artificial sequence

<220>

<221> MUTAGEN

<222> (52)..(66)

<223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>

<221> SIMILAR

<222> (1)..(51)

<223> Identical to residues 267-317 in SEQ ID NO: 1

<220>

<221> SIMILAR

<222> (67)..(109)

<223> Identical to residues 333-375 in SEQ ID NO: 1

<220>

<221> SITE

<222> (73)

<223> Cys or Ser

<220>

<221> SITE

<222> (90)..(91)

<223> Lys Glu or Glu Gly

<400> 16

Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys
1 5 10 15

Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile
20 25 30

Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu
35 40 45

Phe Val Phe Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr
50 55 60

Glu Leu Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser
65 70 75 80

Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly
85 90 95

Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser
100 105

<210> 17

<211> 109

<212> PRT

<213> Artificial sequence

<220>

<221> MUTAGEN

<222> (83)..(97)

<223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>

<221> SIMILAR

<222> (1)..(82)

<223> Identical to residues 267-348 in SEQ ID NO: 1

<220>

<221> SIMILAR

<222> (98)..(109)

<223> Identical to residues 364-375 in SEQ ID NO: 1

<220>

<221> SITE

<222> (73)

<223> Cys or Ser

<220>

<221> SITE

<222> (90)..(91)

<223> Lys Glu or Glu Gly

<400> 17

Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys

1	5	10	15
Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile			
20	25	30	
Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu			
35	40	45	
Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala			
50	55	60	
Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser			
65	70	75	80
Pro Ile Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu			
85	90	95	
Leu Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser			
100	105		

<210> 18
 <211> 109
 <212> PRT
 <213> Artificial sequence

<220>
 <221> MUTAGEN
 <222> (21)..(41)
 <223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>
 <221> SIMILAR
 <222> (42)..(109)
 <223> Identical to residues 307-375 in SEQ ID NO: 1

<220>
 <221> SIMILAR
 <222> (42)..(109)
 <223> Identical to residues 308-375 in SEQ ID NO: 1

<220>
 <221> SITE
 <222> (73)
 <223> Cys or Ser

<220>
 <221> SITE
 <222> (90)..(91)
 <223> Lys Glu or Glu Gly

<400> 18
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys
1 5 10 15

Arg Tyr Pro Leu Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val
20 25 30

Pro Lys Val Ser Ala Ser His Leu Glu Tyr Cys Ser Gly Glu Cys Glu
35 40 45

Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala
50 55 60

Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser
65 70 75 80

Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly
85 90 95

Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser
100 105

<210> 19
<211> 109
<212> PRT
<213> Artificial sequence

<220>
<221> MUTAGEN
<222> (49)..(69)
<223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>
<221> SIMILAR
<222> (1)..(48)
<223> Identical to residues 267-314 in SEQ ID NO: 1

<220>
<221> SIMILAR
<222> (70)..(109)
<223> Identical to residues 336-375 in SEQ ID NO: 1

<220>
<221> SITE
<222> (73)
<223> Cys or Ser

<220>
<221> SITE
<222> (90)..(91)
<223> Lys Glu or Glu Gly

<400> 19
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys
1 5 10 15

Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile
20 25 30

Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu
35 40 45

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
50 55 60

Ala Ser His Leu Glu Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser
65 70 75 80
Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly
85 90 95

Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser
100 105

<210> 20
<211> 109
<212> PRT
<213> Artificial sequence

<220>
<221> MUTAGEN
<222> (79)..(99)
<223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>
<221> SIMILAR
<222> (1)..(78)
<223> Identical to residues 267-345 in SEQ ID NO: 1

<220>
<221> SIMILAR
<222> (100)..(109)
<223> Identical to residues 366-375 in SEQ ID NO: 1

<220>
<221> SITE
<222> (73)
<223> Cys or Ser

<220>
<221> SITE
<222> (90)..(91)
<223> Lys Glu or Glu Gly

<400> 20
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys
1 5 10 15

Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile
20 25 30

Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu
35 40 45

Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala
50 55 60

Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Phe Asn
65 70 75 80

Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser
85 90 95

His Leu Glu Ala Met Val Val Asp Arg Cys Gly Cys Ser
100 105

<210> 21
<211> 109
<212> PRT
<213> Artificial sequence

<220>
<221> MUTAGEN
<222> (84)..(104)
<223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>
<221> SIMILAR
<222> (1)..(83)
<223> Identical to residues 267-349 in SEQ ID NO: 1

<220>
<221> SIMILAR
<222> (105)..(109)
<223> Identical to residues 371-375 in SEQ ID NO: 1

<220>
<221> SITE
<222> (73)
<223> Cys or Ser

<220>
<221> SITE
<222> (90)..(91)
<223> Lys Glu or Glu Gly

<400> 21
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys
1 5 10 15

Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile
20 25 30

Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu
35 40 45

Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala
50 55 60

Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser
65 70 75 80

Pro Ile Asn Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro
85 90 95

Lys Val Ser Ala Ser His Leu Glu Arg Cys Gly Cys Ser
100 105

<210> 22
<211> 254
<212> PRT
<213> Artificial sequence

<220>
<221> SIMILAR
<222> (110)..(124)
<223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>
<221> SIMILAR
<222> (125)..(145)
<223> Diphtheria toxoid P30 epitope (SEQ ID NO: 14)

<220>
<221> SIMILAR
<222> (1)..(109)
<223> 109 C-terminal residues of human and bovine GDF-8
(residues 267-375 in SEQ ID NO: 1)

<220>
<221> SIMILAR
<222> (146)..(254)
<223> 109 C-terminal residues of human and bovine GDF-8
(residues 267-375 in SEQ ID NO: 1)

<220>
<221> SITE
<222> (90)..(91)
<223> Lys Glu or Glu Gly

<220>
<221> SITE
<222> (235)..(236)
<223> Identical to (90)..(91)

<400> 22
Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys
1 5 10 15

Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile
20 25 30

Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu
35 40 45

Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln Ala
50 55 60

Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser
65 70 75 80

Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly
 85 90 95
 Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser Gln Tyr Ile
 100 105 110
 Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Phe Asn Asn Phe
 115 120 125
 Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu
 130 135 140
 Glu Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys
 145 150 155 160
 Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp
 165 170 175
 Ile Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys
 180 185 190
 Glu Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln
 195 200 205
 Ala Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met
 210 215 220
 Ser Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr
 225 230 235 240
 Gly Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser
 245 250

<210> 23
 <211> 160
 <212> PRT
 <213> Artificial sequence

<220>
 <221> MUTAGEN
 <222> (16)..(36)
 <223> Tetanus toxoid P30 epitope (SEQ ID NO: 14)

<220>
 <221> MUTAGEN
 <222> (37)..(51)
 <223> Tetanus toxoid P2 epitope (SEQ ID NO: 13)

<220>
 <221> SIMILAR
 <222> (1)..(15)
 <223> Identical to residues 216-230 of SEQ ID NO: 1

<220>
 <221> SIMILAR
 <222> (52)..(160)

<223> Identical to residues 267-375 of SEQ ID NO: 1

<220>

<221> SITE

<222> (124)

<223> Cys or Ser

<220>

<221> SITE

<222> (141)..(142)

<223> Lys Glu or Glu Gly

<400> 23

Leu Lys Gln Pro Glu Ser Asn Leu Gly Ile Glu Ile Lys Ala Leu Phe
1 5 10 15

Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala
20 25 30

Ser His Leu Glu Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile
35 40 45

Thr Glu Leu Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser
50 55 60

Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp
65 70 75 80

Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly
85 90 95

Glu Cys Glu Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val
100 105 110

His Gln Ala Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr
115 120 125

Lys Met Ser Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile
130 135 140

Ile Tyr Gly Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser
145 150 155 160

<210> 24

<211> 13

<212> PRT

<213> artificial sequence

<400> 13

Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala
1 5 10